

Input file Fbh62112FL.seq; Output File 62112.trans
Sequenc length 2452

																				M	S	G	
CGTGTGTGTGTCCCTGCGGCGCTAAGAAGGGGAGACTGAGGCTGAGGCTGGGGAACATCGGGCAGC																				ATG	AGC	GGC	3
																							9
C	G	L	F	L	R	T	T	A	A	A	R	A	C	R	G	L	V	V	S	23			
TGC	GGG	CTC	TTC	CTG	CGC	ACC	ACG	GCT	GCG	GCT	CGT	GCC	TGC	CGG	GGT	CTG	GTG	GTC	TCT	69			
T	A	N	R	R	L	L	R	T	S	P	P	V	R	A	F	A	K	E	L	43			
ACC	GCG	AAC	CGG	CGG	CTA	CTG	CGC	ACC	AGC	CCG	CCT	GTA	CGA	GCT	TTC	GCC	AAA	GAG	CTT	129			
F	L	G	K	I	K	K	K	E	V	F	P	F	P	E	V	S	Q	D	E	63			
TTC	CTA	GGC	AAA	ATC	AAG	AAG	AAA	GAA	GTT	TTC	CCA	TTT	CCA	GAA	GTT	AGC	CAA	GAT	GAA	189			
L	N	E	I	N	Q	F	L	G	P	V	E	K	F	F	T	E	E	V	D	83			
CTT	AAT	GAA	ATC	AAT	CAG	TTC	TTG	GGA	CCC	GTG	GAA	AAA	TTC	TTC	ACT	GAA	GAG	GTG	GAC	249			
S	R	K	I	D	Q	E	G	K	I	P	D	E	T	L	E	K	L	K	S	103			
TCC	CGA	AAA	ATT	GAC	CAG	GAA	GGG	AAA	ATC	CCA	GAT	GAA	ACT	TTG	GAG	AAA	TTG	AAG	AGC	309			
L	G	L	F	G	L	Q	V	P	E	E	Y	G	G	L	G	F	S	N	T	123			
CTA	GGG	CTT	TTT	GGG	CTG	CAA	GTC	CCA	GAA	GAA	TAT	GGT	GGC	CTG	GGC	TTC	TCC	AAC	ACC	369			
M	Y	S	R	L	G	E	I	I	S	M	D	G	S	I	T	V	T	L	A	143			
ATG	TAC	TCA	AGA	CTA	GGG	GAG	ATC	ATC	AGC	ATG	GAT	GGG	TCC	ATC	ACT	GTG	ACC	CTG	GCA	429			
A	H	Q	A	I	G	L	K	G	I	I	L	A	G	T	E	E	Q	K	A	163			
GCG	CAC	CAG	GCT	ATT	GGC	CTC	AAG	GGG	ATC	ATC	TTG	GCT	GGC	ACT	GAG	GAG	CAG	AAA	GCC	489			
K	Y	L	P	K	L	A	S	G	E	H	I	A	A	F	C	L	T	E	P	183			
AAA	TAC	TTG	CCT	AAA	CTG	GCG	TCC	GGG	GAG	CAC	ATT	GCA	GCC	TTC	TGC	CTC	ACG	GAG	CCA	549			
A	S	G	S	D	A	A	S	I	R	S	R	A	T	L	S	E	D	K	K	203			
GCC	AGT	GGG	AGC	GAT	GCA	GCC	TCA	ATC	CGG	AGC	AGA	GCC	ACA	CTA	AGT	GAA	GAC	AAG	AAG	609			
H	Y	I	L	N	G	S	K	V	W	I	T	N	G	G	L	A	N	I	F	223			
CAC	TAC	ATC	CTC	AAT	GGC	TCC	AAG	GTC	TGG	ATT	ACT	AAT	GGA	GGA	CTG	GCC	AAT	ATT	TTT	669			
T	V	F	A	K	T	E	V	V	D	S	D	G	S	V	K	D	K	I	T	243			
ACT	GTG	TTT	GCA	AAG	ACT	GAG	GTC	GTT	GAT	TCT	GAT	GGA	TCA	GTG	AAA	GAC	AAA	ATC	ACA	729			
A	F	I	V	E	R	D	F	G	G	V	T	N	G	K	P	E	D	K	L	263			
GCA	TTC	ATA	GTA	GAA	AGA	GAC	TTT	GGT	GGA	GTC	ACT	AAT	GGG	AAA	CCC	GAA	GAT	AAA	TTA	789			
G	I	R	G	S	N	T	C	E	V	H	F	E	N	T	K	I	P	V	E	283			
GGC	ATT	CGG	GGC	TCC	AAC	ACT	TGT	GAA	GTC	CAT	TTT	GAA	AAC	ACC	AAG	ATA	CCT	GTG	GAA	849			
N	I	L	G	E	V	G	D	G	F	K	V	A	M	N	I	L	N	S	G	303			
AAC	ATC	CTT	GGA	GAG	GTC	GGA	GAT	GGG	TTT	AAG	GTG	GCC	ATG	AAC	ATC	CTC	AAC	AGC	GGC	909			
R	F	S	M	G	S	V	V	A	G	L	L	K	R	L	I	E	M	T	A	323			
CGG	TTC	AGC	ATG	GGC	AGC	GTC	GTG	GCT	GGG	CTG	CTC	AAG	AGA	TTG	ATT	GAA	ATG	ACT	GCT	969			
E	Y	A	C	T	R	K	Q	F	N	K	R	L	S	E	F	G	L	I	Q	343			
GAG	TAC	GCC	TGC	ACA	AGG	AAA	CAG	TTT	AAC	AAG	AGG	CTC	AGT	GAA	TTT	GGA	TTG	ATT	CAG	1029			
E	K	F	A	L	M	A	Q	K	A	Y	V	M	E	S	M	T	Y	L	T	363			
GAG	AAA	TTT	GCA	CTG	ATG	GCT	CAG	AAG	GCT	TAC	GTC	ATG	GAG	AGT	ATG	ACC	TAC	CTC	ACA	1089			
A	G	M	L	D	Q	P	G	F	P	D	C	S	I	E	A	A	M	V	K	383			
GCA	GGG	ATG	CTG	GAC	CAA	CCT	GGC	TTT	CCC	GAC	TGC	TCC	ATC	GAG	GCA	GCC	ATG	GTG	AAG	1149			
V	F	S	S	E	A	A	W	Q	C	V	S	E	A	L	Q	I	L	G	G	403			

FIGURE 1A

GTG	TTC	AGC	TCC	GAG	GCC	GCC	TGG	CAG	TGT	GTG	AGT	GAG	GCG	CTG	CAG	ATC	CTC	GGG	GGC	1209
L	G	Y	T	R	D	Y	P	Y	E	R	I	L	R	D	T	R	I	L	L	423
TTG	GGC	TAC	ACA	AGG	GAC	TAT	CCG	TAC	GAG	CGC	ATA	CTG	CGT	GAC	ACC	CGC	ATC	CTC	CTC	1269
I	F	E	G	T	N	E	I	L	R	M	Y	I	A	L	T	G	L	Q	H	443
ATC	TTC	GAG	GGA	ACC	AAT	GAG	ATT	CTC	CGG	ATG	TAC	ATC	GCC	CTG	ACG	GGT	CTG	CAG	CAT	1329
A	G	R	I	L	T	T	R	I	H	E	L	K	Q	A	K	V	S	T	V	463
GCC	GGC	CGC	ATC	CTG	ACT	ACC	AGG	ATC	CAT	GAG	CTT	AAA	CAG	GCC	AAA	GTG	AGC	ACA	GTC	1389
M	D	T	V	G	R	R	L	R	D	S	L	G	R	T	V	D	L	G	L	483
ATG	GAT	ACC	GTT	GCC	CGG	AGG	CTT	CGG	GAC	TCC	CTG	GGC	CGA	ACT	GTG	GAC	CTG	GGG	CTG	1449
T	G	N	H	G	V	V	H	P	S	L	A	D	S	A	N	K	F	E	E	503
ACA	GGC	AAC	CAT	GGA	GTT	GTG	CAC	CCC	AGT	CTT	GCG	GAC	AGT	GCC	AAC	AAG	TTT	GAG	GAG	1509
N	T	Y	C	F	G	R	T	V	E	T	L	L	L	R	F	G	K	T	I	523
AAC	ACC	TAC	TGC	TTC	GGC	CGG	ACC	GTG	GAG	ACA	CTG	CTG	CTC	CGC	TTT	GGC	AAG	ACC	ATC	1569
M	E	E	Q	L	V	L	K	R	V	A	N	I	L	I	N	L	Y	G	M	543
ATG	GAG	GAG	CAG	CTG	GTA	CTG	AAG	CGG	GTG	GCC	AAC	ATC	CTC	ATC	AAC	CTG	TAT	GGC	ATG	1629
T	A	V	L	S	R	A	S	R	S	I	R	I	G	L	R	N	H	D	H	563
ACG	GCC	GTG	CTG	TCG	CGG	GCC	AGC	CGC	TCC	ATC	CGC	ATT	GGG	CTC	CGC	AAC	CAC	GAC	CAC	1689
E	V	L	L	A	N	T	F	C	V	E	A	Y	L	Q	N	L	F	S	L	583
GAG	GTT	CTC	TTG	GCC	AAC	ACC	TTC	TGC	GTG	GAA	GCT	TAC	TTG	CAG	AAT	CTC	TTC	AGC	CTC	1749
S	Q	L	D	K	Y	A	P	E	N	L	D	E	Q	I	K	K	V	S	Q	603
TCT	CAG	CTG	GAC	AAG	TAT	GCT	CCA	GAA	AAC	CTA	GAT	GAG	CAG	ATT	AAG	AAA	GTG	TCC	CAG	1809
Q	I	L	E	K	R	A	Y	I	C	A	H	P	L	D	R	T	C	*		622
CAG	ATC	CTT	GAG	AAG	CGA	GCC	TAT	ATC	TGT	GCC	CAC	CCT	CTG	GAC	AGG	ACA	TGC	TGA		1866

GGCAGGGGACAGTGTCCCCCTGCTACCGCCCGCCCCCTACCCATGGCCCGTTGCTGGATGACTGTTACTCTTTTTTTCAGAA
GGTCTTGGGATTATCACAGGTTAAGCCTTTTGTTCCTCGTCTGCACCTGAAGGGTTGTGCGCTGGCCTGGGAGAGCCTC
TTCCAGGTTTTGACCTGCAGGCAGTGCTCTCTAACAGGACCATCACAGCTTCTGAACTGAGCCGGAGAGAGAGAATGGA
ATTGCTGACCCCTGGAAC TGCGGGTATTCTGGTCATTGAGGAGACACCATAGTGGAAACTGGGGCTTATGCTGCTGCC
TCCAGGGTGTGAGGTGGGTGGGGACCTGTGTGTCAGGTGTGGATAGCCATTTCTGCTCAACCACACATTCTCTAAGAAACA
GCTTGAAAGCTCTGTCTGGGTCAATTCATTTAAACTAGAAAGCAGAGGCACTTAAACATGTACCAGGAACCATTTAACAA
AGAATATAAAATGTCACAATCTGTGTACTGT TAAAAAAAAAAAAA

FIGURE 1B

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMM file: /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.26629.seq
Query: 62112

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Acyl-CoA_dh_M 1	Acyl-CoA dehydrogenase, middle domain	153.0	3.5e-42	
Acyl-CoA_dh 1	Acyl-CoA dehydrogenase, C-terminal dom	152.1	9.6e-42	
Acyl-CoA_dh_N 1	Acyl-CoA dehydrogenase, N-terminal dom	73.7	4.2e-19	
Polysac_deacet 1	Polysaccharide deacetylase	-43.7	1.8	

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Acyl-CoA_dh_N	1/1	85	177	29	132	73.7	4.2e-19
Acyl-CoA_dh_M	1/1	179	286	1	106	153.0	3.5e-42
Acyl-CoA_dh	1/1	290	441	1	156	152.1	9.6e-42
Polysac_deacet	1/1	432	580	1	150	-43.7	1.8

Alignments of top-scoring domains:

Acyl-CoA_dh_N: domain 1 of 1, from 85 to 177: score 73.7, E = 4.2e-19
 *->RRvDksgefPalrelikaLgqlGllginvPEeyGGaGad..ylaRFm
 R++D++g+ P e +++L lGl+g+ vPEeyGG+G +++ ++
 62112 85 RKIDQEGKIP--DETLEKLKSLGLFGLQVPPEEYGGGLGFSntMYS-- 126
 LHAQVaalviEElarvcAstgvilsvhssLgqnpilkfGseEQKkkyLpq
 + E+ ++s v+l++h ++g+ +i+ +G+eEQK+kyLp+
 62112 127 -----RLGEIISMDGSITVTLAAHQAIGLKGIIILAGTBEQKAKYLPK 168
 ltsGdliga<-*
 l+sG++i+a
 62112 169 LASGEHIAA 177
 Acyl-CoA_dh_M: domain 1 of 1, from 179 to 286: score 153.0, E = 3.5e-42
 *->AlTEPgAGSDvgSlkTtAekkeGd..dyiLNGsKmWITNGgqAdwyi
 +lTEP +GSD++S++ +A+ d+++yiLNGsK+WITNGg A++++
 62112 179 CLTEPASGSDAASIRSRATLS-EDkkHYILNGSKVWITNGGLANIFT 224
 VlAvT...DpakkvpgkkgitaFlVekdtpGfsiGkKedKLGlRgSdTcE
 V+A+T+ D + + k itaF+Ve+d+ G++ Gk+edKLG+RgS+TcE
 62112 225 VFAKTevvDSDG--SVKDKITAFIVERDFGGVTNGKPEDKLGIRGSNTCE 272
 LiFEDvrvPesniL<-*
 + FE+ ++P +niL
 62112 273 VHFENTKIPVENIL 286
 Acyl-CoA_dh: domain 1 of 1, from 290 to 441: score 152.1, E = 9.6e-42
 *->GkGFkyamkeLdmeRlviAaqalGlaqgaldeAinYakqRkqFGkpl
 G+GFk+am+ L+ +R+ +++ Gl+ + ++ ++Ya RkqF k+l
 62112 290 GDGFKVAMNIIlNSGRFSMGSVVAGLLKRLIEMTAeyACTRkQFNKRL 336

FIGURE 2A

09945326-067101
107E80" 92E54660

```

adfQliQfkLAdMatkLEaaRllvYraAwladr.GedAKEALptskeaam
+f liQ+k+A Ma k ++ +++Y +A d++G + ++s eaam
62112 337 SEFGLIQEKFALMAQKAYVMESMTYLTAGMLDQpGFP-----DCSIEAAM 381

AKlfaseaAmqvadAvQilGGvGYtkdyPverfyRDAkitqIYEGTsEI
+K f+seaA q +++A+QilGG GYt dyP eR +RD +i I EGT+EI
62112 382 VKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTRILLIFEGTNEI 431

grlvIaRall<-*
r Ia + l
62112 432 LRMYIALTGL 441

Polysac_deacet: domain 1 of 1, from 432 to 580: score -43.7, E = 1.8
*->ddksvyLTFDDGPnAApayTprLLDvLkhhkvkATFFviGsnvkdnp
+++++LT + ++ + T+r+ + Lk+ kv + G++ +d
62112 432 LRMYIALTGLQHAG--RILTTRI-HELKQAKVSTVMDTVGRRLRD-- 473

dlarrivkeGHeigNhtwsHPdlt.....tl
+ r v+ G gNH+ HP l+++ ++ ++++ +++ ++ + +
62112 474 -SLGRTVDLG-LTGNHGVVHPSLAdsankfeentycfgrtvettlllrfgK 521

taeqirdeiertneaiiqatggatptlfrpPYGwsetvlsasaklGlaa
t +++ + r+++++i+++g t++l R+ s+s ++Gl+
62112 522 TIMEEQVLVKRVANILINLYG-MTAVLSRA-----SRSIRIGLRN 560

vIWdvDprDWsvragadaivdavlqaa<-*
+ D v ++ v a+lq+
62112 561 H-----DHEVLLANTFCVEAYLQNL 580

```

FIGURE 2B

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMM file: /prod/ddm/seqanal/PFAM/pfam5.4/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.17193.seq

Query: 62112

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Acyl-CoA_dh	Acyl-CoA dehydrogenase	399.8	1.8e-116	1
Polysac_deacet	Polysaccharide deacetylase	-43.7	1	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Acyl-CoA_dh	1/1	85	438	29	394	399.8	1.8e-116
Polysac_deacet	1/1	432	580	1	150	-43.7	1

Alignments of top-scoring domains:

Acyl-CoA_dh: domain 1 of 1, from 85 to 438: score 399.8, E = 1.8e-116

```

*-->RRvDksgefPlrelikaLgklGllginvPEeyGGAgaD..ylaRFmL
R++D++g+ P e +++L lGl+g+ vPEeyGG+G +++ ++
62112 85 RKIDQEGKIP-DETLKLSLGLFGLQVPEEYGGGLGFSntMYS---- 126

HAQVaalviEElarvcAstgvllsvhssLgqnpilrfGseEQkkkyLpql
+ E+ ++s v+l++h ++g+ i+ +G+eEQk+kyLp+l
62112 127 -----RLGEIISMDGSITVTLAAHQAIGLKGIILAGTEEQKAKYLPKL 169

tsGdligafAlTEPgAGSDvgSikTtAekkeGd..dyiLNGsKmWITNGg
    
```

FIGURE 2C

09454650
063104
101E80"92E54650

```
62112 170 +sG++i+af+lTEP +GSD++Si+ +A+ d+++yilNGsK+WITNGg
ASGEHIAAFCLTEPASGSDAASIRSRTLs-EDKkHYILNGSKVWITNGG 218
qAdwyiVlAvT...DpakkvpgkkgitaFlVekdtpGfsiGkKedKLGLR
A++++V+A+T+ D + + k itaF+Ve+d+ G++ Gk+edKLG+R
62112 219 LANIFTVFAKTeVVDSdg--SVKDKITAFIVERDFGGVTNGKPEDKLGIr 266
gSdTcELiFEDvrvPesniLGeEGeGFkyaMktLdmeRlgiAaqalGiaq
gS+TcE+ FE+ ++P +niLGe G+GFk+aM+ L+ +R+ +++ G++
62112 267 GSNTCEVHFENTKIPVENILGEVGDGFKVAMNILNSGRFSMGSVVAGLLK 316
gAldeAinYAkqRkqFGkplaefQliQfkLadMatkLEaarllvYraAwl
+ ++ +++YA RkqF k+l ef liQ+k+A MA k ++ +++Y +A
62112 317 RLIEMTAeyACTRKQFNKRLSEFGLIQEKFALMAQKAYVMESMTYLTAGM 366
adr.GedAKEALptskeAAMAKlfAseiAmkvatdAvQilGGvGYtkdyp
d++G + ++s eAAM+K f+se+A + +++A+QilGG GYt dyP
62112 367 LDQpGFP-----DCSIEAMVKVFSSEAAWQCVSEALQILGGLGYTRDYP 411
verfyRDAkitqiYEGTseIQrlvIaR<-*
eR +RD +i I EGT+EI r Ia
62112 412 YERILRDTRILLIFEgTNEILRMylAL 438

Polysac_deacet: domain 1 of 1, from 432 to 580: score -43.7, E = 1
*->ddksvyLTfDDGPnAApayTprlLDvLkKhkvkATFFviGsnvkdnP
+++++LT + ++ + T+r+ + Lk+ kv + G++ +d
62112 432 LRMylALtGLQHAG--RILTTRI-HELKQAKVSTVMDTVGRRLRD-- 473
dlarriVkeGHeigNhtwsHPdlt.....tl
+ r v+ G gNH+ HP l+++ ++ ++++ +++ ++ + +
62112 474 -SLGRTVDLG-LTGNHGvvHPSLAdsankfeentycfgrtvetlllrfgK 521
taeqirdeiertneaiiqatggatptlfrpPYGwsetvlsasaklGltA
t +++ + r+++++i+++g t++l R+ s+s ++Gl+
62112 522 TIMEEQVLVKRVANILINLYG-MTAVLSRA-----SRSIRIGLRN 560
vLWdvDprDWsvragadaivdavlqaa<-*
+ D v ++ v a+lq+
62112 561 H-----DHEVLLANTFCVEAYLQNL 580
```

FIGURE 2D

00045326 083101
T01E80" 92E5H660

TxP expression: 30K array

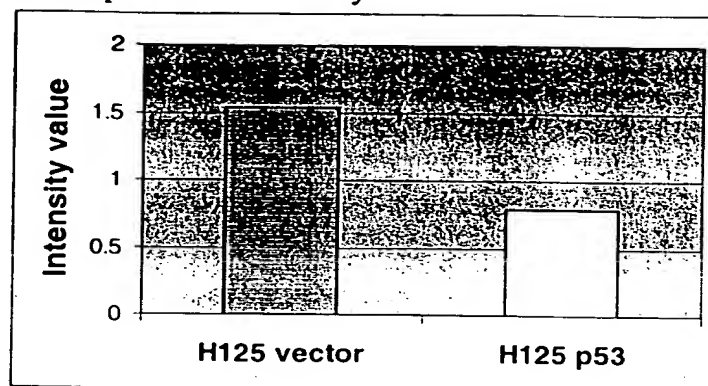


FIGURE 3A

Taqman expression

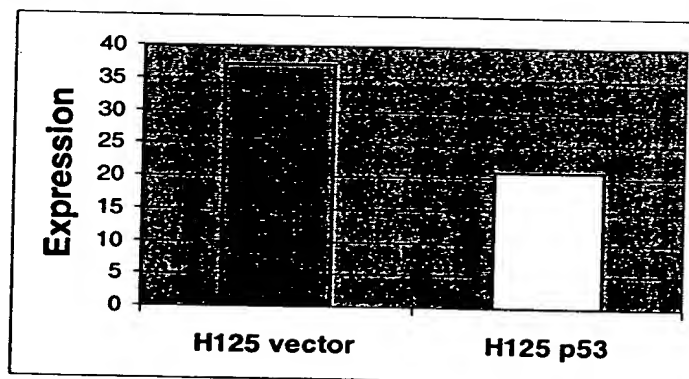


FIGURE 3B

0945326 063404

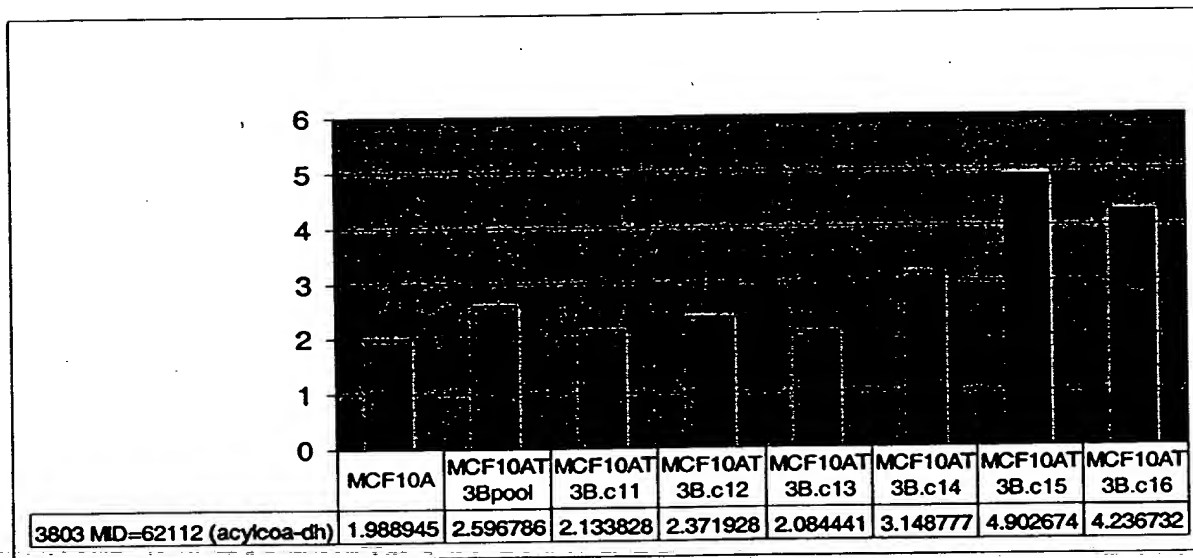


FIGURE 4

101E30" 92E51650

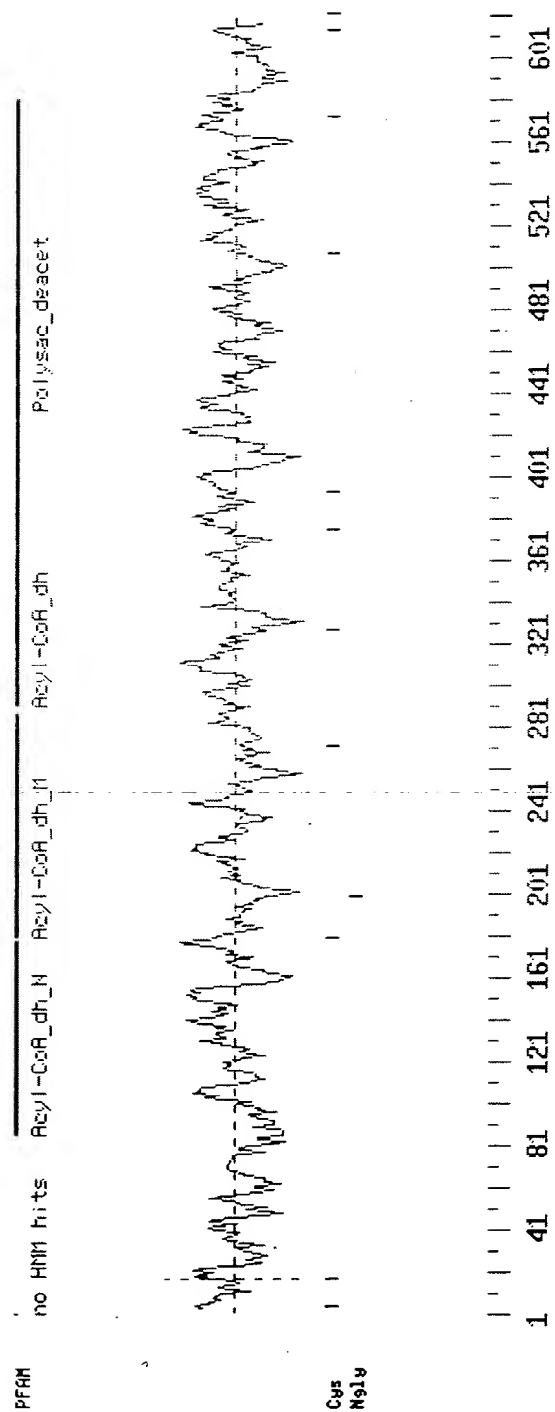


FIGURE 5